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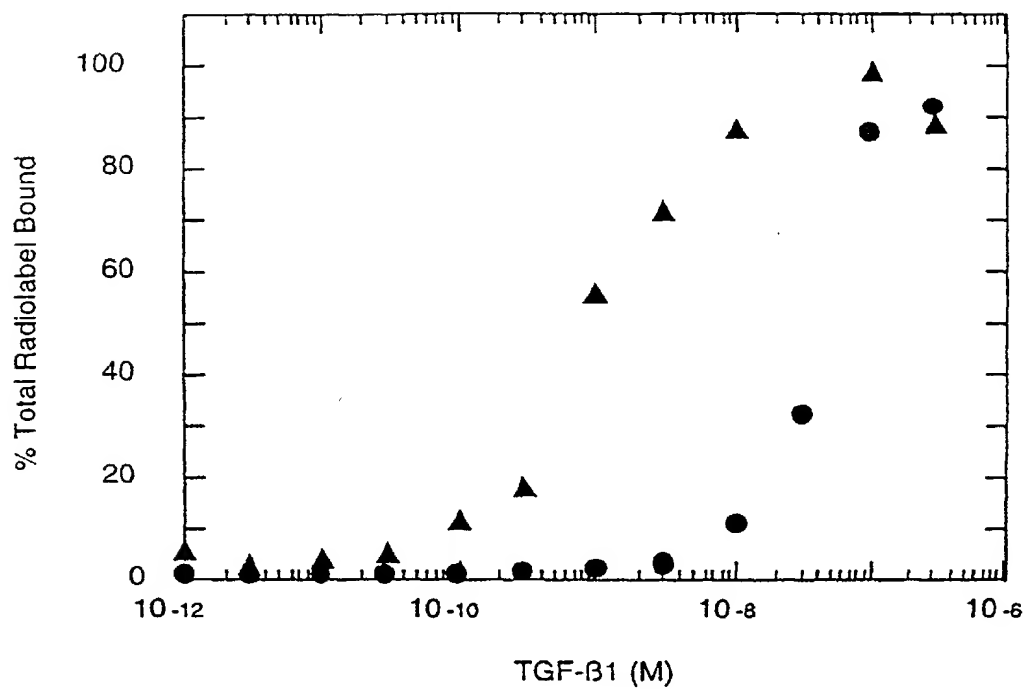
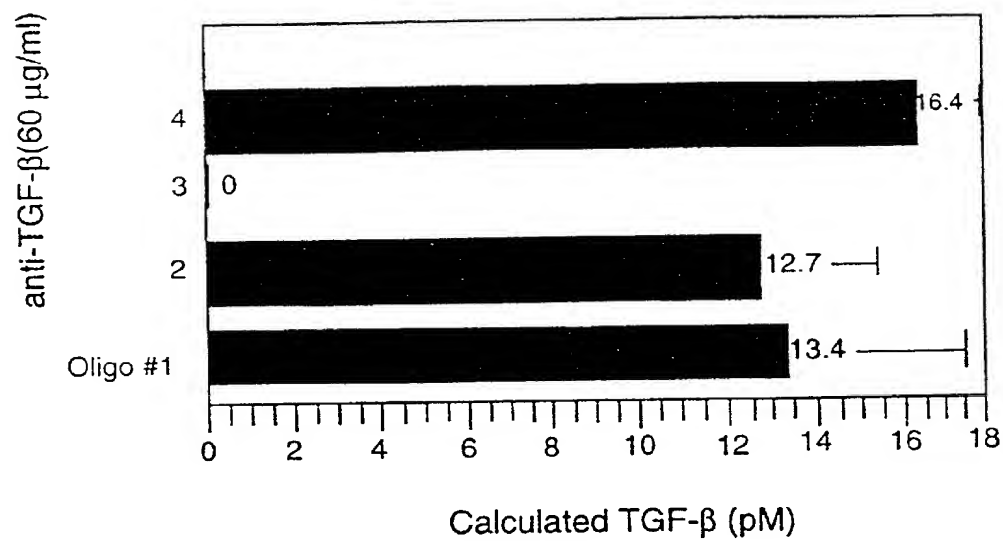


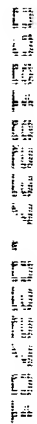
FIGURE 1

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Oligos (0.1 μ M)+
TGF- β 1 (10pM)

FIGURE 2

[illegible][illegible][illegible]

[illegible]

36t

ACCGTACG
GGCAATCC
GACATGTA
GCTCTA
GCG
GCG
AT
CG
AT
5'CG[3'T]

SEQ ID NO: 173

20t

C^TT^T
T^TG^TC^T
C^TC^TG^TA^T
C^TC^TC^TG^TG^T
G-C
G-C
G-C

5'TGGGA-G-C[3'T]

SEQ ID NO: 172

41 t

5' T A C T C A G T C G C A G T G C A T A A G C
[3'T] A T G A G T C G C A G T G C A T A A G C

SEQ ID NO: 174

FIGURE 4

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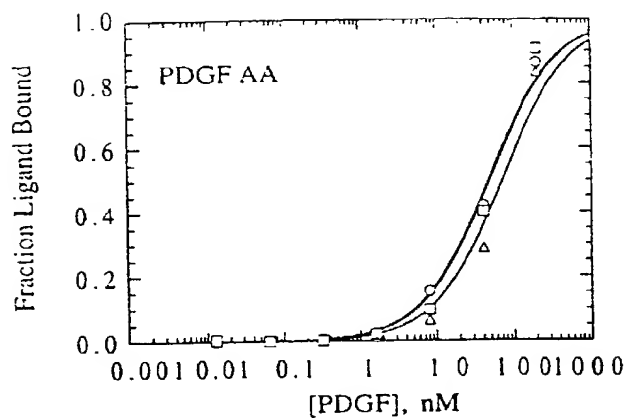


Figure 5A

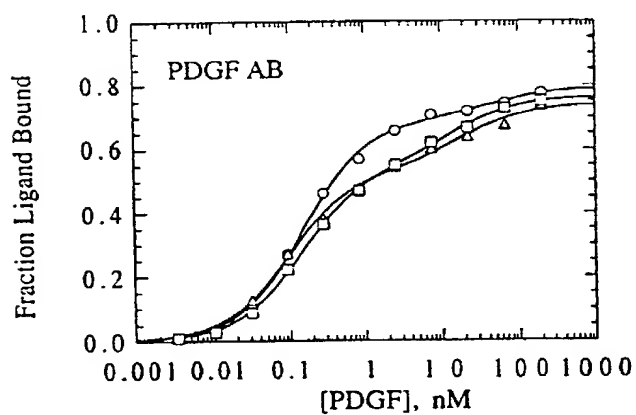


Figure 5B

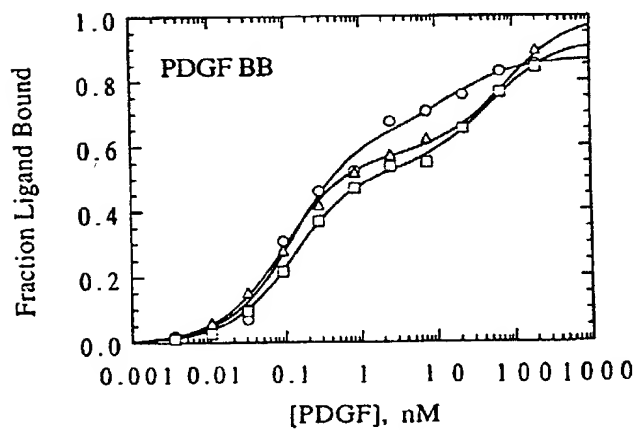


Figure 5C

SUBSTITUTE SHEET (RULE 26)

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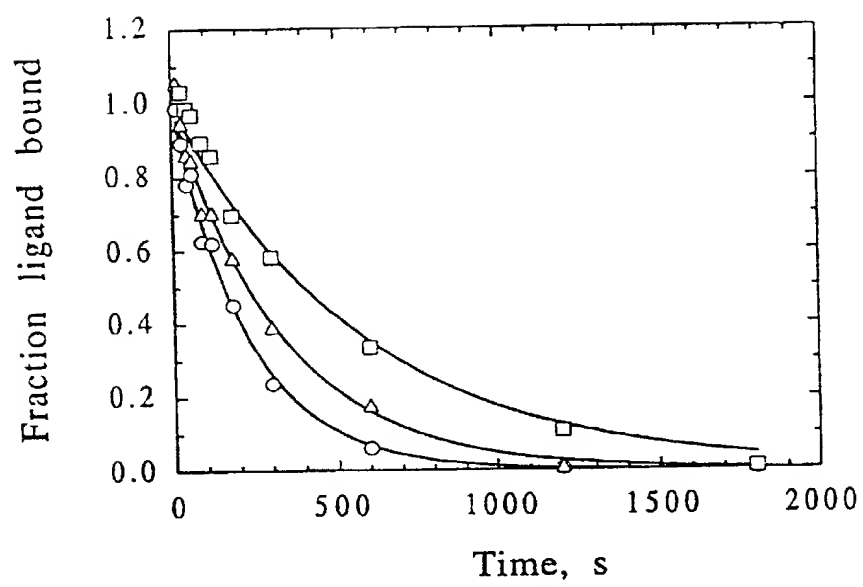


FIGURE 6

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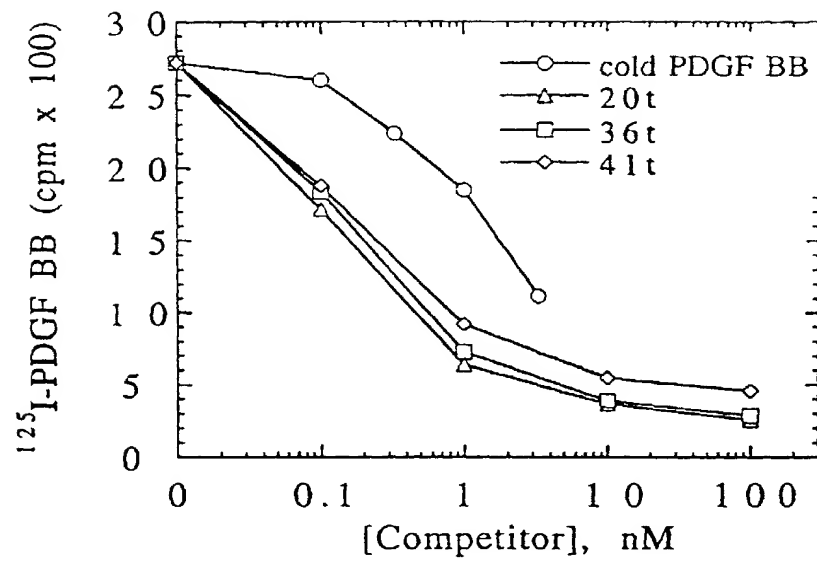


FIGURE 7

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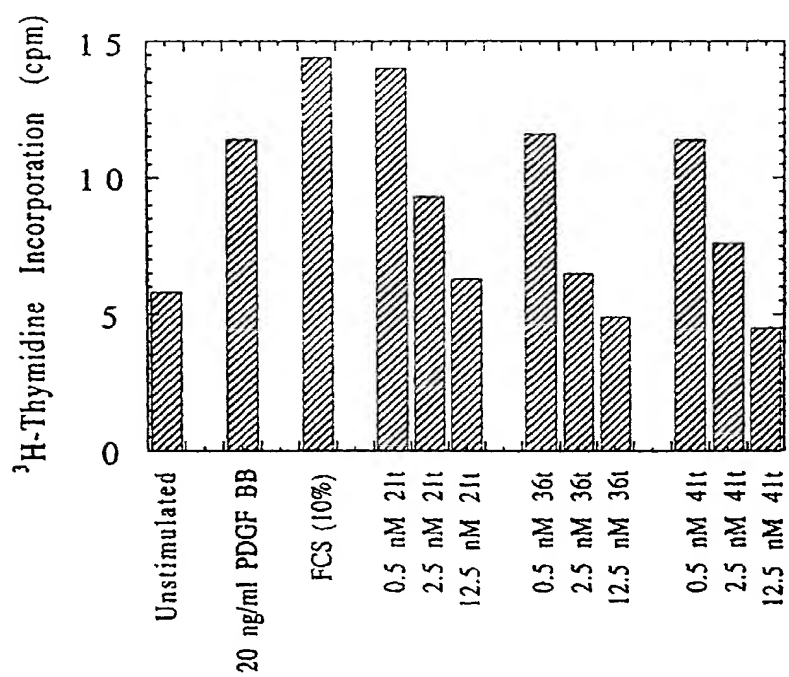
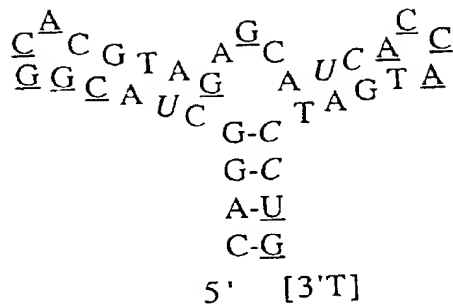
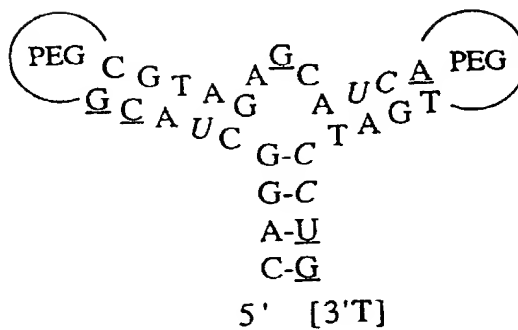


FIGURE 8

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 $K_d=0.065$ nM

SEQ ID NO: 175

 $K_d=0.097$ nM

SEQ ID NO: 176

FIGURE 9

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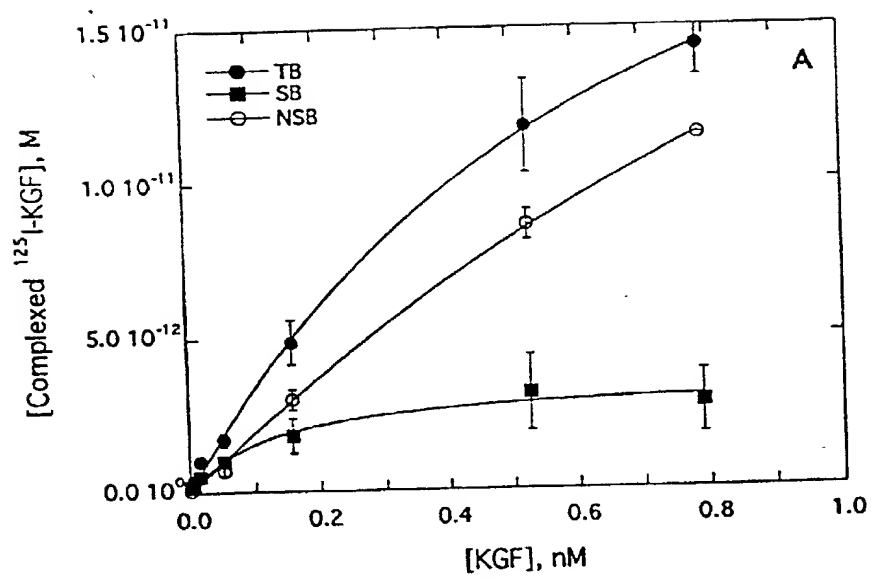


FIGURE 10A

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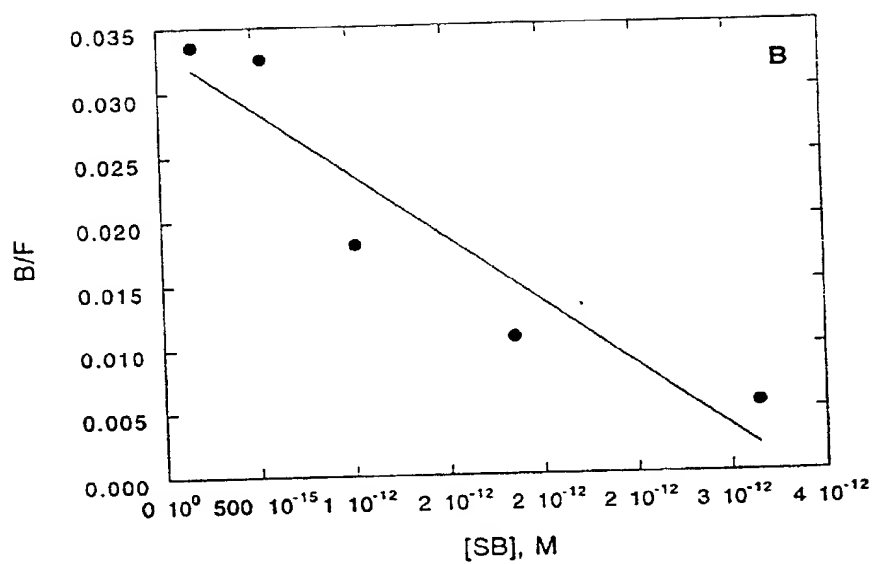


FIGURE 10B

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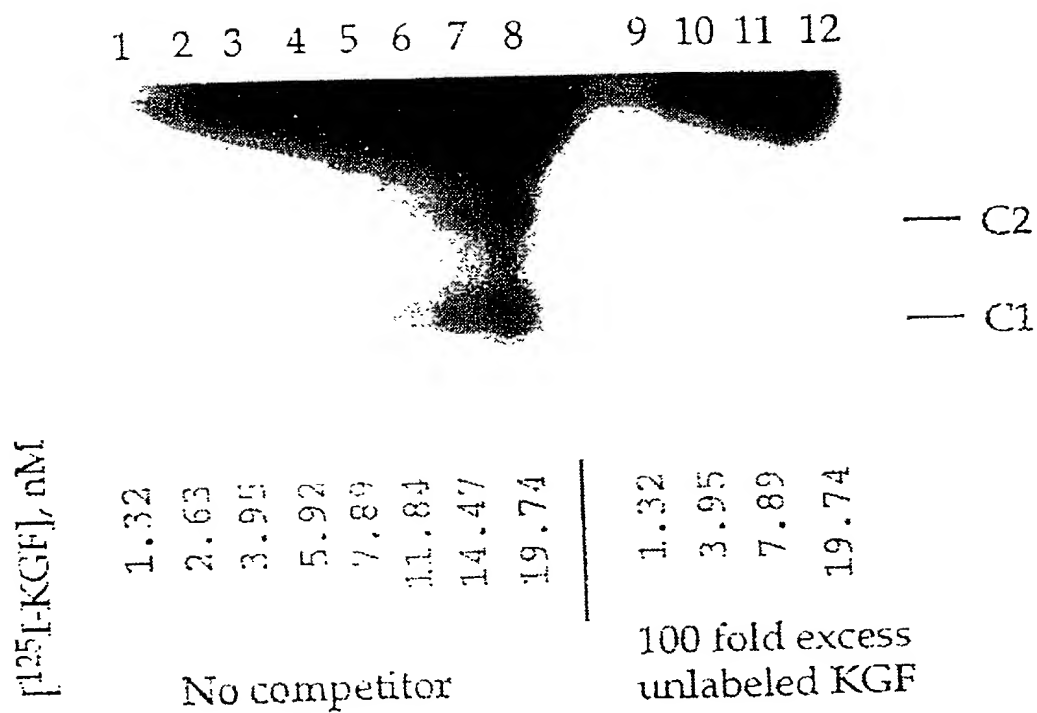


FIGURE 11

Class 1

SEQ ID NO:	Clone	K _d , nM	K _i , nM	
231	*14P	0.001	3.3	gagaga
232	*6P	0.05	1.3	gagagaga
233	*15P	0.07	6.7	gagagagaga
234	*56P	0.07	0.3	gagagagaga
235	*26P	0.23	6.7	gagagagaga
236	37P	0.46		gagagagaga
237	*16P	0.83		gagagagaga
238	42P	0.9		gagagagaga
239	31P	1.0		gagagagaga
240	35P	1.1		gagagagaga
241	54P	1.23		gagagagaga
242	51P	1.27		gagagagaga
243	2P	1.77		gagagagaga
244	24P	2.02		gagagagaga
245	60P	2.1		gagagagaga
246	23P	2.52		gagagagaga
247	5P	2.53		gagagagaga
248	8P	2.63		gagagagaga
249	29P	3.24		gagagagaga
250	7P	3.69		gagagagaga
251	45P	4.7		gagagagaga
252	Consensus			gagagagaga

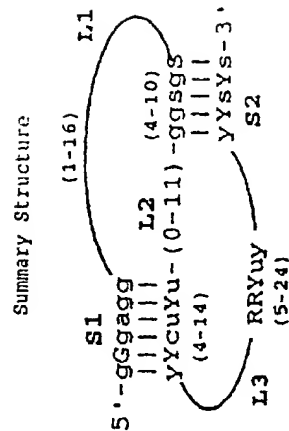


FIGURE 12A

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Class 2

SEQ ID NO:	Clone	K _d , nM	K _i , nM	
230	*13P	0.03	10.0	
254	*50P	0.12		
247	38P	0.33	0.2	
227	10P	0.47	10.0	
226	9P	0.83		
256	53P	0.7		
253	49P	1.0		
250	43P	1.13	16.7	
260	57P	1.2		
248	41P	1.44		
241	27P	1.52		
235	20P	2.05		
258	55P	2.52		
261	58P	2.52		
221	3P	4.47		
236	21P	ND		
242	28P	ND		
269	Consensus			

Summary Structure

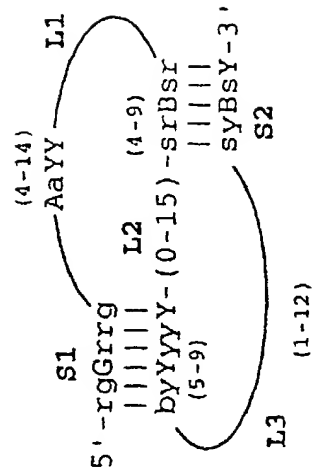


FIGURE 12B

Class 1							
SEQ ID NO:	Clone	Kd, nM	Ki, nM	UAAAG	CCGCCG	gacgac	UUAUUA
195	14N	0.4	2.0	CAACUA	GCAGUAACCCGACGUCGCGGACGA	gacgac	UUAUUA
199	25N	0.9		UAAAGUAACCCG		CCCGAC	UUAUUA
191	4N	0.7	21.3	CAACAA	GUGGUGGCGGACGA	gacgac	UUAUUA
189	1N	0.5	16.7	UAAAG	ACAAGUCGACAAAG	gacgac	UUAUUA
205	36N	8.27		CAGUC	ACAGUGC	gacgac	UUAUUA
203	34N	0.8		CAAC	CCGCCG	UUAUUA	UUAUUA
207	42N	0.8	266.7	CA CU	UGAACGA	gacgac	UUAUUA
196	16N	1.4		YAA	RCRR	gacgac	UUAUUA
	Consensus						UUAUUA

Summary Structure

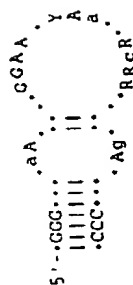


FIGURE 12C

Class 2							
SEQ ID NO	Clone	Kd, nM	Ki, nM				
209	47N	1.8		ACGAGGUAAGAGGAAA	CAGC	CCUU	GUGGagacga <u>cucgcccya</u>
198	24N	1.2		<u>gacgaugcg</u>	GUUGGAAGA	CCCGUCG	AAUGUGAC <u>ACUGGGcca</u>
202	29N	0.43	13.3	AGAAAGAUCCA	GGAAACAGCGAA	UCCGU	CCGdAcgac <u>UCUGccga</u>
204	35N	2.3		<u>ugcgggCUUAG</u>	GGAAA	CUGAU	Ucagacgac <u>UCUGccya</u>
192	6N	0.7	26.7	<u>acgaugcggc</u>	AGGGAGCAA	CCGUCACGU	agacgacuc <u>gcccgga</u>
190	2N	0.8	66.7	GGCGA	AAAGAA	gggaggacgaugcgCGGGAAGGUC	CGAA <u>GACCI</u>
211	54N	5.3		GGG	CGAAG	gggaggacgaugcgAGAACCAACAG	AGCCCCCUGUGGUU
271	Consensus			CGAA	yGa	CUCagacgacucgccga	yGay

Summary Structure

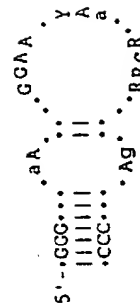
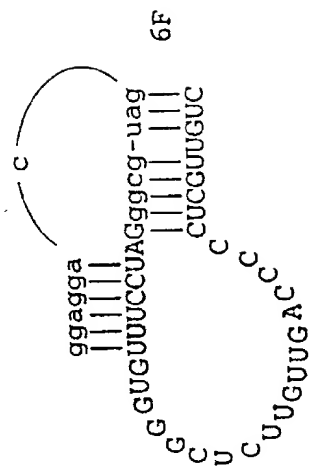


FIGURE 12D

6F gggaggacgaugcggGAUCCUUGUGGGUCUUGUGAGACCCUUGUGUCCCCCagagacacucgccccga

SEQ ID NO: 223



14F gggaggacgaugcggUGGUCUCCCAUUCUAACUUCUCCAUUGUAUUGGGCCagagacacucgccccga

SEQ ID NO: 231

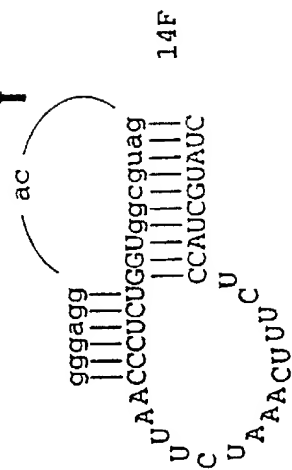


FIGURE 13